

CERTIFICATE OF EXPRESS MAIL
Express Mailing No. EL 839286487 US
Date of Deposit: May 14, 2001

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
THOMAS SPIES AND
VERONIKA SPIES

Group Art Unit: 1644

Serial No.: Unknown

Examiner: DIBRINO. M

Filed: May 14, 2001

Atty. Dkt. No.: FHCC:003USC1

For: CELL STRESS REGULATED HUMAN
MHC CLASS 1 GENE

REQUEST FOR TRANSFER OF SEQUENCE LISTING UNDER 37 C.F.R. § 1.821(e)

BOX SEQUENCE

Commissioner for Patents
Washington, D.C. 20231

Commissioner:

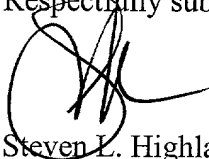
Pursuant to 37 C.F.R. § 1.821(e), Applicants respectfully request that the sequence information previously submitted in parent application ("parent application"), U.S. Serial No. 09/303,161 filed April 29, 1999, be transferred to and used in the above-referenced patent application ("instant application"). Only one computer readable sequence listing was submitted to the U.S. Patent and Trademark Office in the parent application. The sequence information in the instant application is identical to the sequence information contained in the previously-filed computer readable sequence listing in the parent application. It is understood that the U.S. Patent and Trademark Office will make the necessary change in application number and filing date of

the computer readable form that will be used for the instant application. A paper copy of the sequence listing is included in the originally-filed specification of the instant application.

Applicants request the transfer of the previously-filed computer readable sequence listing from the parent application to the instant application is in lieu of filing a duplicate computer readable sequence listing.

No fee is believed to be due in connection with the filing of this document; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be deemed necessary for any reason relating to this document, the Commissioner is hereby authorized to deduct said fee from Fulbright & Jaworski Account No.: 50-1212/10008888/SLH.

Respectfully submitted,



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Austin, Texas 78701
(512) 536-3184

Date: May 14, 2001

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Fred Hutchinson Cancer Research Center, Inc.
 (B) STREET: 1100 Fairview Avenue North, Mailstop c2M-027
 (C) CITY: Seattle
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 (F) POSTAL CODE (ZIP): 98109

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 (D) STATE: Washington
 (E) COUNTRY: USA
 (F) POSTAL CODE (ZIP): 98112

(A) NAME: Veronika Spies
 (B) STREET: 2429 E. Aloha
 (C) CITY: Seattle
 (D) STATE: Washington
 (E) COUNTRY: USA
 (F) POSTAL CODE (ZIP): 98112

(ii) TITLE OF INVENTION: CELL STRESS REGULATED HUMAN MHC CLASS I GENE

(iii) NUMBER OF SEQUENCES: 16

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/029,044
 (B) FILING DATE: 29-OCT-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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 CTGAAGAGAG AAAAGTCCCC AGGGAATAAA CACAACACTG CACCCAGTGG AGCATTACC 11400
 CATTTCCCTC TTTTCTCCAG AGCTCGTGAG CCTGCAGGTC CTGGATCAAC ACCCAGTTGG 11460
 GACGAGTGAC CACAGGGATG CCACACAGCT CGGATTTCAG CCTCTGATGT CAGCTCTTGG 11520
 GTCCACTGGC TCCACTGAGG GCGCCTAGAC TCTACAGCCA GGCGGCTGGA ATTGAATTCC 11580
 CTGCCTGGAT CTCACAAGCA CTTTCCCTCT TGGTGCCTCA GTTTCCTGAC CTATGAAACA 11640
 GAGAAAATAA AAGCACTTAT TTATTGTTGT TGGAGGCTGC AAAATGTTAG TAGATATGAG 11700
 GCATTTGCAG CTGTGCCATA TT 11722

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Gly Leu Gly Pro Val Phe Leu Leu Leu Ala Gly Ile Phe Pro Phe
 1 5 10 15
 Ala Pro Pro Gly Ala Ala Ala Glu Pro His Ser Leu Arg Tyr Asn Leu
 20 25 30
 Thr Val Leu Ser Trp Asp Gly Ser Val Gln Ser Gly Phe Leu Ala Glu
 35 40 45

Val	His	Leu	Asp	Gly	Gln	Pro	Phe	Leu	Arg	Tyr	Asp	Arg	Gln	Lys	Cys	50	55	60	
Arg	Ala	Lys	Pro	Gln	Gly	Gln	Trp	Ala	Glu	Asp	Val	Leu	Gly	Asn	Lys	65	70	75	80
Thr	Trp	Asp	Arg	Glu	Thr	Arg	Asp	Leu	Thr	Gly	Asn	Gly	Lys	Asp	Leu	85	90	95	
Arg	Met	Thr	Leu	Ala	His	Ile	Lys	Asp	Gln	Lys	Glu	Gly	Leu	His	Ser	100	105	110	
Leu	Gln	Glu	Ile	Arg	Val	Cys	Glu	Ile	His	Glu	Asp	Asn	Ser	Thr	Arg	115	120	125	
Ser	Ser	Gln	His	Phe	Tyr	Tyr	Asp	Gly	Glu	Leu	Phe	Leu	Ser	Gln	Asn	130	135	140	
Val	Glu	Thr	Glu	Glu	Trp	Thr	Val	Pro	Gln	Ser	Ser	Arg	Ala	Gln	Thr	145	150	155	160
Leu	Ala	Met	Asn	Val	Arg	Asn	Phe	Leu	Lys	Glu	Asp	Ala	Met	Lys	Thr	165	170	175	
Lys	Thr	His	Tyr	His	Ala	Met	His	Ala	Asp	Cys	Leu	Gln	Glu	Leu	Arg	180	185	190	
Arg	Tyr	Leu	Glu	Ser	Ser	Val	Val	Leu	Arg	Arg	Arg	Val	Pro	Pro	Met	195	200	205	
Val	Asn	Val	Thr	Arg	Ser	Glu	Ala	Ser	Glu	Gly	Asn	Ile	Thr	Val	Thr	210	215	220	
Cys	Arg	Ala	Ser	Ser	Phe	Tyr	Pro	Arg	Asn	Ile	Thr	Leu	Thr	Trp	Arg	225	230	235	240
Gln	Asp	Gly	Val	Ser	Leu	Ser	His	Asp	Thr	Gln	Gln	Trp	Gly	Asp	Val	245	250	255	
Leu	Pro	Asp	Gly	Asn	Gly	Thr	Tyr	Gln	Thr	Trp	Val	Ala	Thr	Arg	Ile	260	265	270	
Cys	Gln	Gly	Glu	Glu	Gln	Arg	Phe	Thr	Cys	Tyr	Met	Glu	His	Ser	Gly	275	280	285	
Asn	His	Ser	Thr	His	Pro	Val	Pro	Ser	Gly	Lys	Val	Leu	Val	Leu	Gln	290	295	300	
Ser	His	Trp	Gln	Thr	Phe	His	Val	Ser	Ala	Val	Ala	Ala	Ala	Ala	Ala	305	310	315	320
Ala	Ile	Phe	Val	Ile	Ile	Ile	Phe	Tyr	Val	Arg	Cys	Cys	Lys	Lys	Lys	325	330	335	
Thr	Ser	Ala	Ala	Glu	Gly	Pro	Glu	Leu	Val	Ser	Leu	Gln	Val	Leu	Asp	340	345	350	

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Gln His Pro Val Gly Thr Ser Asp His Arg Asp Ala Thr Gln Leu Gly
 355 360 365

Phe Gln Pro Leu Met Ser Ala Leu Gly Ser Thr Gly Ser Thr Glu Gly
 370 375 380

Ala
 385

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGCCATGGG GCTGGGCCGG GTCCTGCTGT TTCTGGCCGT CGCCTTCCCT TTTGCACCCC 60
 CGGCAGCCGC CGCTGAGCCC CACAGTCTTC GTTACAACCT CATGGTGCTG TCCCAGGATG 120
 AATCTGTGCA GTCAGGGTTT CTCGCTGAGG GACATCTGGA TGGTCAGCCC TTCCTGCGCT 180
 ATGACAGGCA GAAACGCAGG GCAAAGCCCC AGGGACAGTG GGCAGAAGAT GTCCTGGGAG 240
 CTAAGACCTG GGACACAGAG ACCGAGGACT TGACAGAGAA TGGGCAAGAC CTCAGGAGGA 300
 CCCTGACTCA TATCAAGGAC CAGAAAGGAG GCTTGCATTC CCTCCAGGAG ATTAGGGTCT 360
 GTGAGATCCA TGAAGACAGC AGCACCAGGG GCTCCCGGCA TTTCTACTAC GATGGGGAGC 420
 TCTTCCTCTC CAAAACCTG GAGACTCAAG AATCGACAGT GCCCCAGTCC TCCAGAGCTC 480
 AGACCTTGGC TATGAACGTC ACAAATTTCT GGAAGGAAGA TGCCATGAAG ACCAAGACAC 540
 ACTATCGCGC TATGCAGGCA GACTGCCTGC AGAAACTACA GCGATATCTG AAATCCGGGG 600
 TGGCCATCAG GAGAACAGTG CCCCCATGG TGAATGTCAC CTGCAGCGAG GTCTCAGAGG 660
 GCAACATCAC CGTGACATGC AGGGCTTCCA GCTTCTATCC CCGGAATATC ACACTGACCT 720
 GGCCTCAGGA TGGGGTATCT TTGAGCCACA ACACCCAGCA GTGGGGGGAT GTCCTGCCTG 780
 ATGGGAATGG AACCTACCAG ACCTGGGTGG CCACCAGGAT TCGCCAAGGA GAGGAGCAGA 840
 GGTTACCTG CTACATGGAA CACAGCGGGA ATCACGGCAC TCACCCTGTG CCCTCTGGGA 900
 AGGTGCTGGT GCTTCAGAGT CAACGGACAG ACTTTCCATA TGTTTCTGCT GCTATGCCAT 960
 GTTTTGTAT TATTATTATT CTCTGTGTCC CTTGTTGCAA GAAGAAAACA TCAGCGGCAG 1020
 AGGGTCCAGA GCTTGTGAGC CTGCAGGTCC TGGATCAACA CCCAGTTGGG ACAGGAGACC 1080
 ACAGGGATGC AGCACAGCTG GGATTTGAGC CTCTGATGTC AGCTACTGGG TCCACTGGTT 1140

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CCACTGAGGG CGCCTAGACT CTACAGCCAG GCGGCCAGGA TTCAACTCCC TGCCTGGATC 1200
 TCACCAGCAC TTTCCCTCTG TTTCTGACC TATGAAACAG AAAATAACAT CACTTATTTA 1260
 TTGTTGTTGG ATGCTGCAAA GTGTTAGTAG GTATGAGGTG TTTGCTGCTC TGCCACGTAG 1320
 AGAGCCAGCA AAGGGATCAT GACCAACTCA ACATTCCATT GGAGGCTATA TGATCAAACA 1380
 GCAAATTGTT TATCATGAAT GCAGGATGTG GGCAAACCTCA CGACTGCTCC TGCCAACAGA 1440
 AGGTTTGCTG AGGGCATTCA CTCCATGGTG CTCATTGGAG TTATCTACTG GGTCACTAG 1500
 AGCCTATTGT TTGAGGAATG CAGTCTTACA AGCCTACTCT GGACCCAGCA GCTGACTCCT 1560
 TCTTCCACCC CTCTTCTTGC TATCTCCTAT ACCAATAAAT ACGAAGGGCT GTGGAAGATC 1620
 AGAGCCCTTG TTCACGAGAA GCAAGAAGCC CCCTGACCCC TTGTTCCAAA TATACTCTTT 1680
 TGTCTTTCTC TTTATTCCCA CGTTCGCCCT TTGTTGAGTC CAATACAGGG TTGTGGGGCC 1740
 CTTAACAGTG CCATATTAAT TGGTATCATT ATTTCTGTTG TTTTGTGTTT TGTTTTGTTT 1800
 TTTGTTTTTG AGACAGAGTC TCACTCGTCA CCCAGGCTGC AGTTCACTGG TGTGATCTCA 1860
 GCTCACTGCA ACCTCTGCCT CCCAGGTTCA AGCACTTCTC GTACCTCAGA CTCCCGATAG 1920
 CTGGGATTAC AGACAGGCAC CACCACACCC AGCTAATTTT TGTATTTTTT GTAGAGACGG 1980
 GGTTCGCCCA AGTTGACCAG CCCAGTTTCA AACTCCTGAC CTCAGGTGAT CTGCCTGCCT 2040
 TGGCATCCCA AAGTGCTGGG ATTACAAGAA TGAGCCACCG TGCCTGGCCT ATTTTATTAT 2100
 ATTGTAATAT ATTTTATTAT ATTAGCCACC ATGCCTGTCC TATTTTCTTA TGTTTTAATA 2160
 TATTTAATA TATTACATGT GCAGTAATTA GATTATCATG GGTGAACCTT ATGAGTGAGT 2220
 ATCTGGTGA TGA CTCTCC TGACCAGCCC AGGACCAGCT TTCTTGTCAC CTTGAGGTCC 2280
 CCTCGCCCCG TCACACCGTT ATCGATTACT CTGTGTCTAC TATTATGTGT GCATAATTTA 2340
 TACCGTAAAT GTTACTCTT TAAATAAAAA AAAAAAAAAA 2380

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Gly Leu Gly Arg Val Leu Leu Phe Leu Ala Val Ala Phe Pro Phe
 1 5 10 15
 Ala Pro Pro Ala Ala Ala Glu Pro His Ser Leu Arg Tyr Asn Leu
 20 25 30

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Met Val Leu Ser Gln Asp Glu Ser Val Gln Ser Gly Phe Leu Ala Glu
 35 40 45
 Gly His Leu Asp Gly Gln Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg
 50 55 60
 Arg Ala Lys Pro Gln Gly Gln Trp Ala Glu Asp Val Leu Gly Ala Lys
 65 70 75 80
 Thr Trp Asp Thr Glu Thr Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu
 85 90 95
 Arg Arg Thr Leu Thr His Ile Lys Asp Gln Lys Gly Gly Leu His Ser
 100 105 110
 Leu Gln Glu Ile Arg Val Cys Glu Ile His Glu Asp Ser Ser Thr Arg
 115 120 125
 Gly Ser Arg His Phe Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn
 130 135 140
 Leu Glu Thr Gln Glu Ser Thr Val Pro Gln Ser Ser Arg Ala Gln Thr
 145 150 155 160
 Leu Ala Met Asn Val Thr Asn Phe Trp Lys Glu Asp Ala Met Lys Thr
 165 170 175
 Lys Thr His Tyr Arg Ala Met Gln Ala Asp Cys Leu Gln Lys Leu Gln
 180 185 190
 Arg Tyr Leu Lys Ser Gly Val Ala Ile Arg Arg Thr Val Pro Pro Met
 195 200 205
 Val Asn Val Thr Cys Ser Glu Val Ser Glu Gly Asn Ile Thr Val Thr
 210 215 220
 Cys Arg Ala Ser Ser Phe Tyr Pro Arg Asn Ile Thr Leu Thr Trp Arg
 225 230 235 240
 Gln Asp Gly Val Ser Leu Ser His Asn Thr Gln Gln Trp Gly Asp Val
 245 250 255
 Leu Pro Asp Gly Asn Gly Thr Tyr Gln Thr Trp Val Ala Thr Arg Ile
 260 265 270
 Arg Gln Gly Glu Glu Gln Arg Phe Thr Cys Tyr Met Glu His Ser Gly
 275 280 285
 Asn His Gly Thr His Pro Val Pro Ser Gly Lys Val Leu Val Leu Gln
 290 295 300
 Ser Gln Arg Thr Asp Phe Pro Tyr Val Ser Ala Ala Met Pro Cys Phe
 305 310 315 320
 Val Ile Ile Ile Ile Leu Cys Val Pro Cys Cys Lys Lys Lys Thr Ser
 325 330 335

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Ala Ala Glu Gly Pro Glu Leu Val Ser Leu Gln Val Leu Asp Gln His
 340 345 350

Pro Val Gly Thr Gly Asp His Arg Asp Ala Ala Gln Leu Gly Phe Gln
 355 360 365

Pro Leu Met Ser Ala Thr Gly Ser Thr Gly Ser Thr Glu Gly Ala
 370 375 380

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACTGGGGAAC AAGGTTTATA TGAGA 25

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TGTCACCCGT CTTCTACAGG ACCC 24

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGGCCATGG GGCTGGG 17

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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ATCTGAGATG TCGGTCC

17

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGTTCTTGTC CCTTTGCCCCG TGTGC

25

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AACCCTTCCC TTACCCCCGT CGTAG

25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TATGTAAAC GACGGCCAGT TTCACCTGTG ATTCCTCTT CCCCA

45

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGTCTTTTCA ATCCCCGTCT CTCGTCCAGT ATCGACAAAG GACAT

45

(2) INFORMATION FOR SEQ ID NO: 13:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TATGTAAAAC GACGGCCAGT TTCGGAATG GAGAAGTCAC

40

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CGAGAGGAGA GGGAGGTAA CCAGTATCGA CAAAGGACAT

40

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TATGTAAAAC GACGGCCAGT GTTCCTCTCC CTCCTTAGA

40

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AAAAAGTCCC TTTCACGACC ACCAGTATCG ACAAAGGACA T

41

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